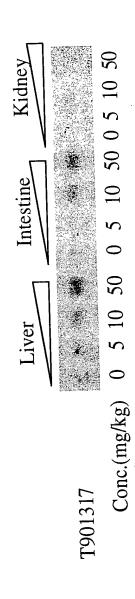
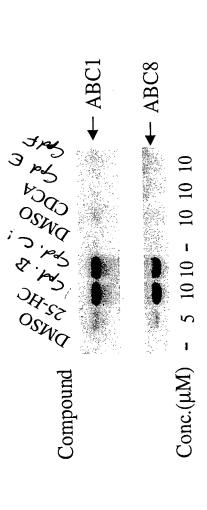
LXR Agonist Compound A Activates the Expression of SSE



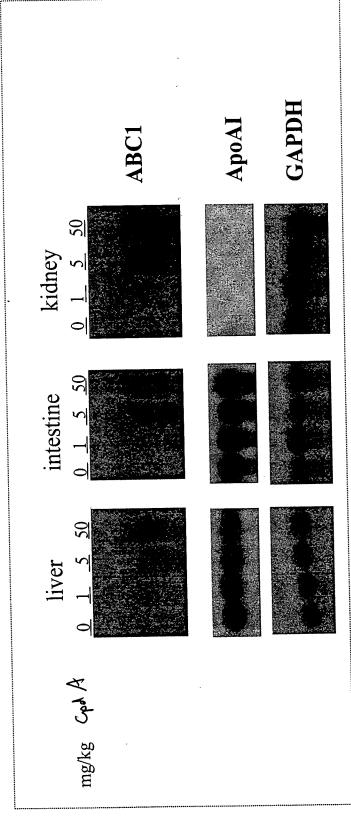
# Oxysterol and LXR Agonists Activate the Expression of Cholesterol Transporters, ABC1 and ABC8

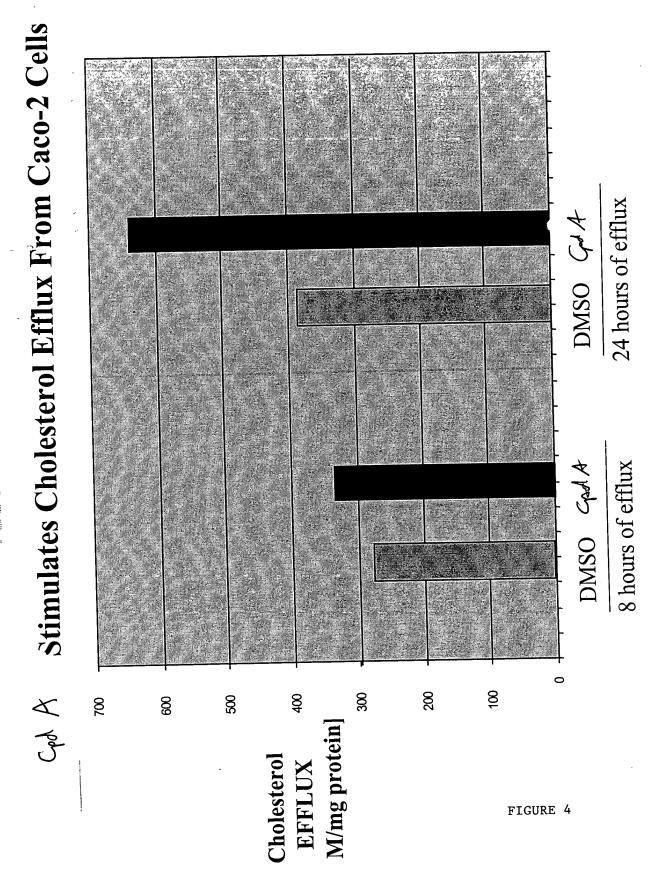


LXR agonist: 'God B, C

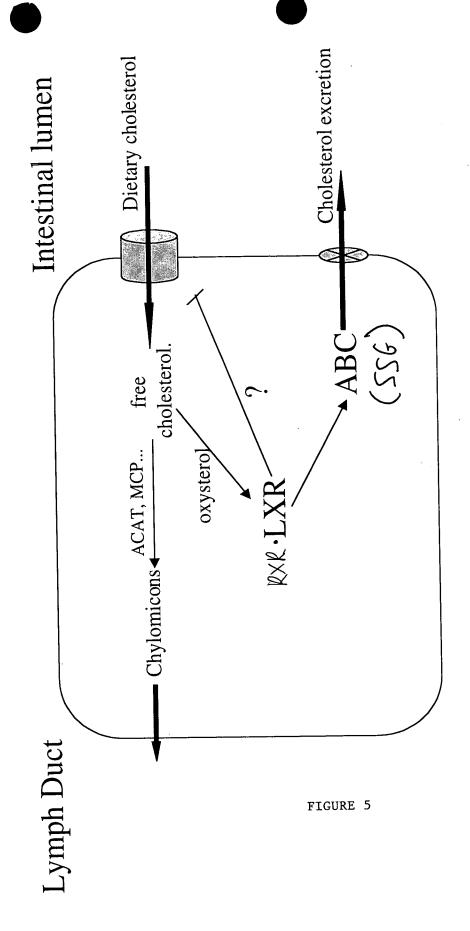
FXR agonist: Cpd E, F

## Induction of ABC1 in Liver, Intestine and Kidney of C57BL/6 Mice by LXRa Agonist God A





# How Does LXR Regulate Cholesterol Absorption? -A Working Model -



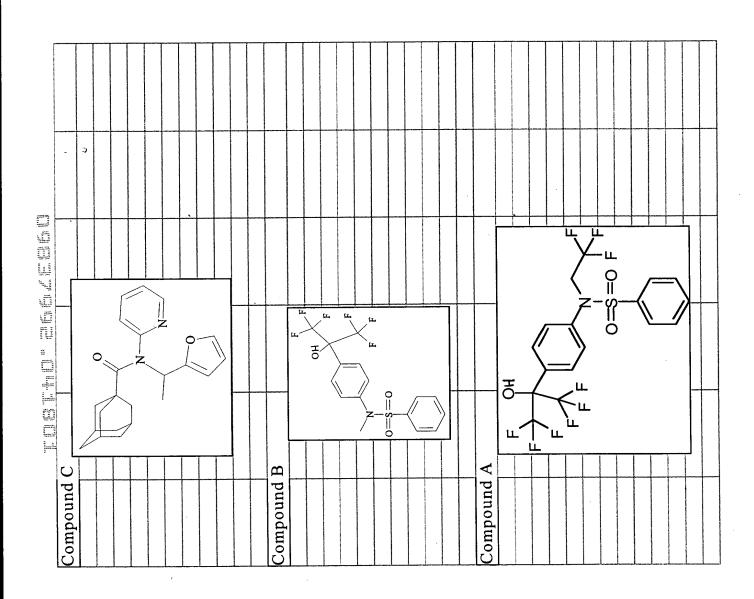


FIGURE 6

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TACATICCAAAAATATIGCAGIGAGATICTIGTAGICAATGAGTICTACGGACTGAATITICACTTOTGGCAGCACTAATGAGAAATGTGTGCCTTCACTCAAGAAATTGATGAGAAAACCTGCCCAGG T F Q K Y C S E I L V V N E F Y G L N F T C G S S N V S V T T N P M C A F T Q G I Q F I E K T C P G> S K L G V L L R R V T R N L V R N K L A V I T R L L Q N L I M G L F L L F F V L R V R S N V L K G A> AYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEF> IETSKR V QM IESAYKKSAICHKTLKNIERMKHLKTLPM V P F K T K D S P G V F> K K V E A V M A E L S L S H V A D R L I G N Y S L G G I S T G E R R R V S I A A Q L L Q D P K V M L> GITTGATGAGCCAACCACAGGCCTGGACTGCTAAATCAGATTGTCGTCCTCGTGGTACTGGCTGCGAAATTGTGGTTCTCACCATTCACCAGCCCGTTCTGAGCTTTTTCAGCTCTTTGAGAAAAATTGCCAT FDEPTTG LDCMTAR LDC WTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAI> L S F G E L I F C G T P A E M L D F F N D C G Y P C P E H S N P F D F Y M D L T S V D T Q S K E R B> 1650 M G D L S S L T P G G S M G L> 300 CCAAGINAACAGAGGCTCCCAGAGGGGCCCCCGGAGGCCTCACAGGCTCCTCCATGCCTCCTACAGGCTCAGCGTCAGGGGCCCTGGTGGGACATCACTTGCCGGCAGCAGTGGAC Q V N R G S Q S S L E G A P A T A P E P H S L G I L H A S Y S V S H R V R P W W D I T S C R Q Q W T> R Q I L K D V S L Y V E S G Q I M C I L G S S G S G K T T L L D A M S G R L G R A G T F L G E V Y V> N G R A L R R E Q F Q D C F S Y V L Q S D T L L S S L T V R E T L H Y T A L L A I R R G N P G S F Q> AATAGAAACCICCAAGAGGGCCAGATGAATGCCGCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATGAAAGAATGAAACACGTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAGAATGTTTTT 1350 150 GICAGGIGGAGCAGGCAGICIGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGACCACCAGAAATTTGCCCAGCTTTGCTGCTGTTGGCAATGGTGACCTCTCATCTTTGACCCCGGAGGGTCCATGGGTCT GAAGAGGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAACTGATTGGCAACTACAGCGTTGGGGGGCATTTCCACGGGTGAGCGGCCGGGTCTCCATCGCAGCCCAGCTGCTCCAGGATCCTAAGGTCATGCT ATSRFTMNFLILYSFIPALVILGIVVFKIRDHLISR X> tigctcttacaactitgcagggacaigtggttatttggaaatttgtggccgagcggacccaagaaigtaaaataatattcalaaactaatggg 1875 2025 675

### Alignment of Human and Mouse SSG Protein Sequences

hSSG.pro	MGDLSSLTPG GSMGLQVNRG SQSSLEGAPA TAPEP-HSLG ILHASYSVSH	49 .
mSSG.pro	MGELPFLSPE GARGPHINRG SLSSLEQGSV TGTEARHSLG VLHVSYSVSN	50
hSSG.pro	RVRPWWDITS CROOWTROIL KDVSLYVESG QIMCILGSSG SGKTTLLDAM	99
mSSG.pro	RVGPWWNIKS COOKWDRQIL KDVSLYIESG QIMCILGSSG SGKTTLLDAI	100
hSSG.pro	SGRLGRAGTF LGEVYVNGRA LRREQFODCF SYVLOSDTLL SSLTVRETLH	149
mSSG.pro	SGRLRRTGTL EGEVFVNGCE LRRDQFODCF SYVLOSDVFL SSLTVRETLR	150
hSSG.pro	YTALLAIRRG NPGSFOKKVE AVMAELSLSH VADRLIGNYS LGGISTGERR	199
mSSG.pro	YTAMLALCRS SADFYNKKVE AVMTELSLSH VADQMIGSYN FGGISSGERR	200
hSSG.pro	RVSIAAQLLQ DPKVMLFDEP TTGLDCMTAN QIVVLLVELA RRNRIVVLTI	249
mSSG.pro	RVSIAAQLLQ DPKVMMLDEP TTGLDCMTAN QIVLLLAELA RRDRIVIVTI	250
hSSG.pro	HOPRSELFOL FDKIAILSFG ELIFCGTPAE MLDFFNDCGY PCPEHSNPFD	299
mSSG.pro	HOPRSELFOH FDKIAILTYG ELVFCGTPEE MLGFFNNCGY PCPEHSNPFD	300
hSSG.pro	FYMDLTSVDT QSKEREIETS KRVQMIESAY KKSAICHKTL KNIERMKHLK	349
mSSG.pro	FYMDLTSVDT QSREREIETY KRVQMLECAF KESDIYHKIL ENIERARYLK	350
hSSG.pro	TLPMVPFKTK DSPGVFSKLG VLLRRVTRNL VRNKLAVITR LLQNLIMGLF	399
mSSG.pro	TLPMVPFKTK DPPGMFGKLG VLLRRVTRNL MRNKQAVTMR LVQNLIMGLF	400
hSSG.pro	LLFFVLRVRS NVLKGAIQDR VGLLYQFVGA TPYTCMLNAV NLFPVLRAVS	449
mSSG.pro	LIFYLLRVQN NTLKGAVQDR VGLLYQLVGA TPYTCMLNAV NLFPMLRAVS	450
hSSG.pro	DQESQDGLYQ KWQMMLAYAL HVLPFSVVAT MIFSSVCYWT LGLHPEVARF	499
mSSG.pro	DQESQDGLYH KWQMLLAYVL HVLPFSVIAT VIFSSVCYWT LGLYPEVARF	500
hSSG.pro	GYFSAALLAP HLIGEFLTLV LLGIVONPNI VNSVVALLSI AGVLVGSGFL	549
mSSG.pro	GYFSAALLAP HLIGEFLTLV LLGIVONPNI VNSIVALLSI SCLLIGSGFI	550
hSSG.pro	RNIQEMPIPF KIISYFTFQK YCSEILVVNE FYGLNFTCGS SNVSVTTNPM	599
mSSG.pro	RNIQEMPIPL KILGYFTFQK YCCEILVVNE FYGLNFTCGG SNTSMLNHPM	600
hSSG.pro	CAFTOGIOFI EKTCPGATSR FTMNFLILYS FIPALVILGI WYFKIRDHLI	649
mSSG.pro	CAITOGVOFI EKTCPGATSR FTANFLILYG FIPALVILGI VIFKVRDYLI	650
hSSG.pro	SR	651
mSSG.pro	SR	652

Reference Number: 6711 Stanford RH Panel: TNG4 Lowest LOD Reported: 6 Chromosome Value: 0

### Results for HT

Submitted

001000000000001000100

# SHGCNAME CHROM# LOD\_SCORE DIST.(cRs)

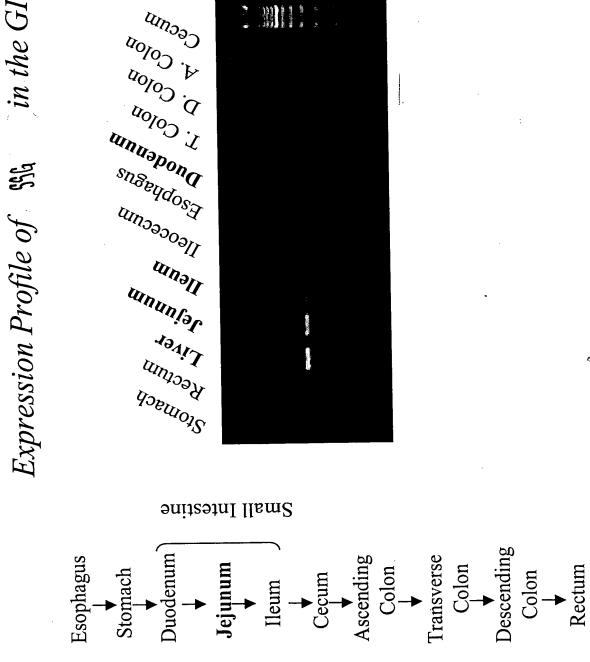
1 SHGC-36672 2 7.52 35 001000000000R0100Q100

001000000000101000100

3 SHGC-699 2 6.03 48 9 000000100000011000100

The number of markers searched was 32440.

in the GI Tract



LICHE II

## is Predominantly Expressed in the Liver and Small Intestine Human

SUMYAT SitsoT u<sub>aa/d</sub>s S. Intestine PBL Prostate Colon S. Muscle placenta b<sup>gUCL6g8</sup> Brain Heart Kidney Liver

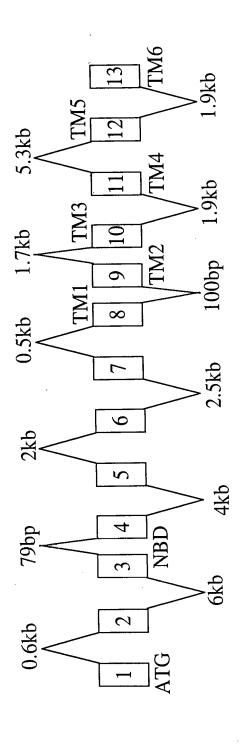
### is Selectively Expressed in the Liver and Small Intestine Mouse !

S. Intestine Sing Spleen Lung Spleen Spleen Spleen Spleen Brain Thymus S. Muscle Jestis Skin

Mouse Multiple Tissue RT-PCR

# cDNA Cloning and Genomic Organization of 𝘘ﮔੈੈੈ।

- The predicted human and mouse proteins share 80% identity and is 28% identical to Drosophila Brown
- Human ABCG5 contains 13 exons and spans at least 25kb of genomic DNA



### Human SSG nucleotide sequence—13 Exons

Exan 1 GTCAGGTGGAGCAGGCAGTCTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGA GGGTCCGGCCACCAGAAAATTTGCCCAGCTTTGCTGCCTGTTGGCCATGGGTGACCTCTC ATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCT TGCCACCGCCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTA CAC<mark>C</mark>ÕÕCGCGTGAGGCCCTGGTGGGACATCACATCTTGCCGGCAGCAGTGGAC CAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCT ĞGGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCG TGTATGŢGAACGGCCGGGCGCTGCGCCGGGAGCAGTT ACACCGCGCTGCTGGCCATCCGCCGCGGCAATCCCGGCTCCTTCCA GAAGAAGGTGC**A**ĞĞCCĞTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGAT ATTTCCACGGGTGAGCGGCGCCGGGTCTCCATCGCAGC TAAGGTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTG CATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGGC CCTGAGCTTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGGA TGACTGCGGTTACCCTTGTCCTGAACATTCAAACCCTTTTGACTTCTATATĞĞÄCCTGAC GTCAGTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGAT AGAATCTGCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAAT GAAACACCTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAAGATTCTCCTGGAGTTTT CTCTAAACTGGGTGTTCTCCTGAGGAGGTGACAAGAAACTTGGTGAGAAATAAGCTGGC AGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTTTTCTTCGTTCT GCGGGTCCGAAGCAATGTGCTAAAGGGTGCTATCCAGGACCGC GTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAATCTGTTTCČČČČĞTGCT GCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAAGTGGCAGATGATGCT CCCTTCAGCGTTGTTGCCACCATGATTTTCAGCAGTGT GTGCTACTGGĞĞĞĞĞĞĞGĞGCTTACATCCTGAGGTTGCCCGATTTGGATATTTTTCTGCTGC TCTCTTGGCCCCCCACTTAATTGGTGAATTTCTAACTCTTGTGCTACTTGGTATCGTCCA AAATCCAAATATAGTCAACAGTGTAGTGGCTCTGCTGCTCCATTGCGGGGGTGCTTGTTGG ATCTGGATTCCTCAGAÃČAŤACAAGAAATGCCCATTCCTTTTAAAATCATCAGTTATTT TACATTCCAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTT CACTTGTGECAGCTCAAATGTTTCTGTGACAACTAATCCAATGTGTGCCTTCACTCAAGG AATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGATTCACAATGAACTTTCT

	Exon number	exon size	5' splicing site	3' splicing site	Intron size
,	1 ·			GCGTCAGgtaaggcag	~600bp
	2	124	cctttaaagCCACCGC	AGCTCAGgtaagcttg	~6kb
	3	137	gcccgcagGCTCCGG	CCTGCAGgtgggcgcg	79bp
	4	103	ctcctgcagAGCGACA	AAGGTGGgtgcagccc	~4kb
	5	129	tgcaggtggAGGCCGT	GATCCTAgtaagtggc	~2kb
	6	140	tgctggcagAGGTCAT	TTTTCAGgtaagaggt	~2.5kb
	7	130	tctggtcagCTCTTTG	TTCTATAgtaagtttt	~0.5kb
	8	214	aacttttagTGGACCT	TCCTGAGgtaagaggc	100bp
	9	206	tgttttcagGAGAGTG	AATCTGTgtaagtgcc	~1.7kb
	10	139	catccccagTTCCCGT	GCTACTGgtgaggggtt	~1.9kb
	11	186	cttttctagGACGCTG	<b>TCCTCAGgtaagatat</b>	~5.3kb
	12	113	tttcttaagAAACATA	ACTTGTGgtaagtatt	~1.2kb
	13		ccttgacagGCAGCTC		
	Total		-		~25.9kb

Exonic sequences in capital letter

FIGURE 14B (2 of 2)